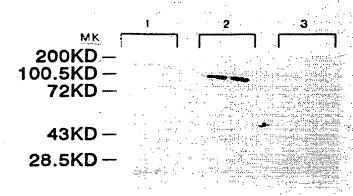


FIGURE 1



1 - anti- EGFr PoAB RK-2 2 - Cyt-356 MoAB/RAM 3 - RAM WO 94/09820 PCT/US93/10624

08/466381

FIGURE 2A

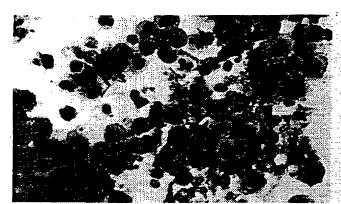


FIGURE 2B

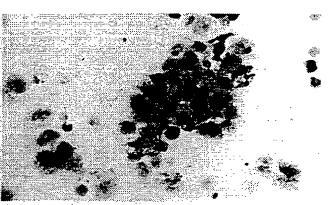


FIGURE 2C

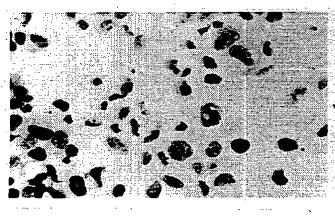
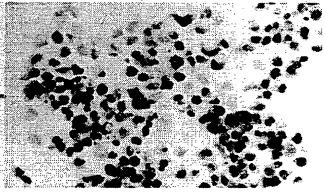


FIGURE 2D



18. 466381

FIGURE 3A

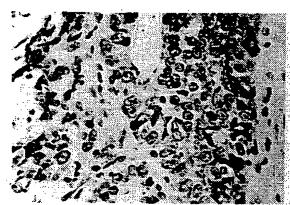


FIGURE 3B

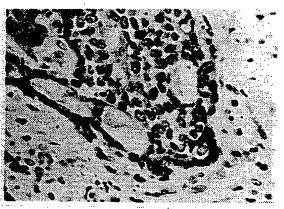


FIGURE 3C

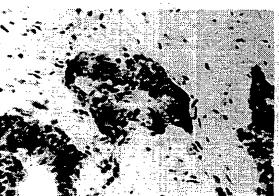
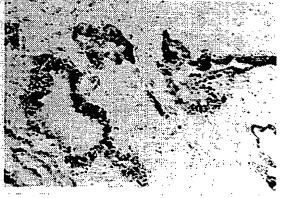


FIGURE 3D



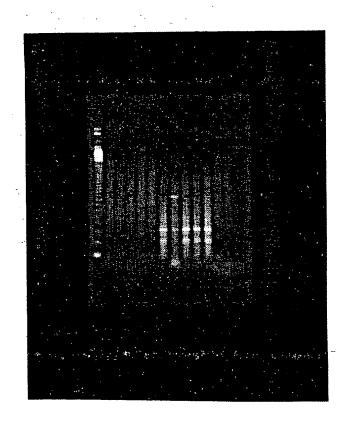
4/48

FIGURE 4

43.0

28.5

5/48 FIGURE 5



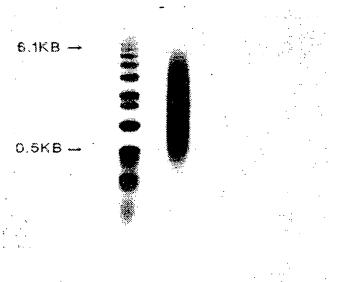
⁰⁸. 466381

FIGURE 6A FIGURE 6B

⁰⁸/466381

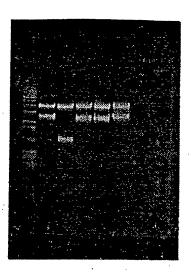
7/48

FIGURE 7



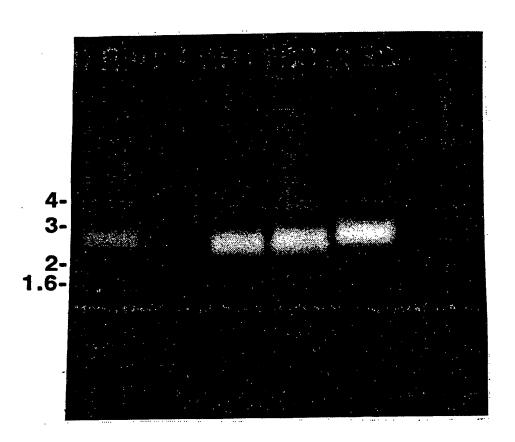
8/48

FIGURE 8

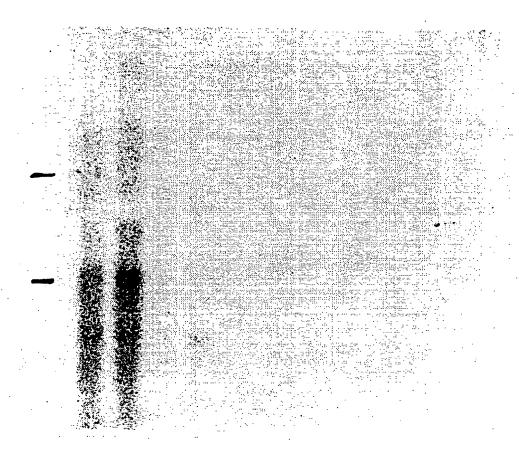


¹⁸/466381

9/48 FIGURE 9



10/48 FIGURE 10



11/48 FIGURE 11

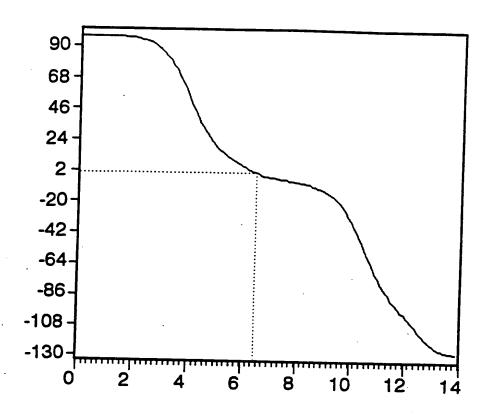
1 2 3
9.5__
7.5__
4.4__
2.4__
1.4__

12/48

FIGURE 12A

FIGURE 12B

13/48 FIGURE 13



lв

FIGURE 14-1

sednence. 750. the complete residues is: **PMSANTIGEN** Done on sequence Analysis done on Total number of

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codes. Sequence shown with conformation

14/48

are given conformation Ø in residues more or Ŋ of stretch Consecutive overlined.

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回	F	IX	IX	II	U	IX	团	H	नि
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臼	IH	IX	नि	E	田	H	H	धि	lFJ
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团	王	臼	E	旧	मि	IX	IH	巨	मि
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ပ	IX	E	IE	न	IH	IX	I	H	II
ပ	H	回	IE	IH	II	IX	H	 됸	II
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凹	IX	回	H	IX	II	II	阳	ि	ပ
451	481	511	541	571	601	631	661	691	721

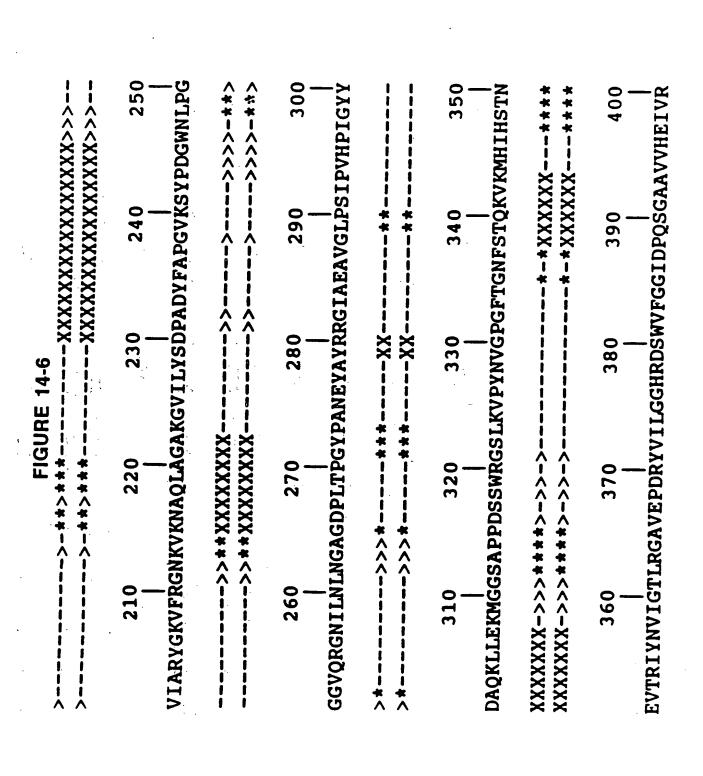
FIGURE 14-4

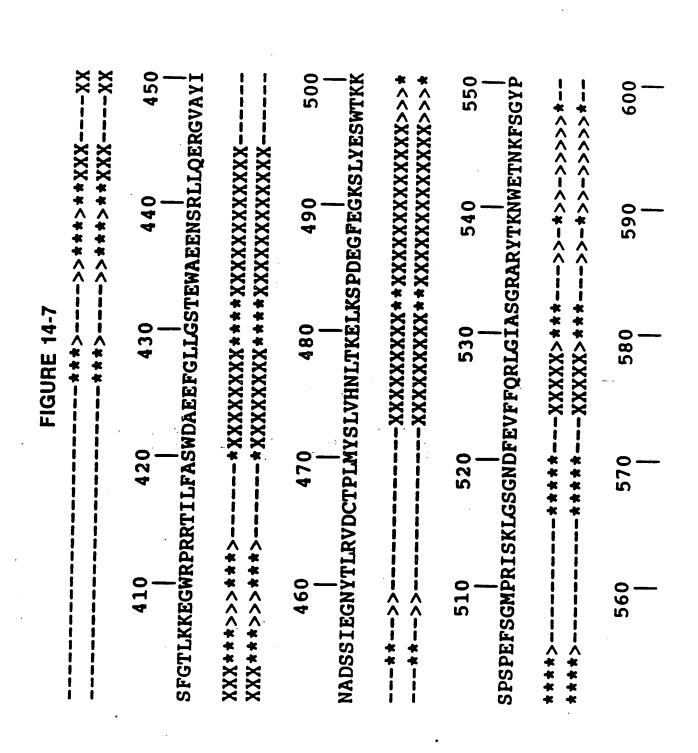
Semi-graphical output.

<pre>Helical conformation: X Extended conformation: - Turn conformation: > Coil conformation: *</pre>	10 20 30 40 50	MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT	X<************************************	60 70 80 90 100	nitpkhnmkafldelkaenikkflynftqiphlagteqnfqlakqiqsqw
	conformation: X Extended conformation: conformation: > Coil conformation:	<pre>conformation: X</pre>	<pre>conformation: X</pre>	: : : : : :	: : uo o

150 __*X_XXXXXXXXXXX******---<<---KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG 200 ^^****^^----X**^*-**YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI** 140 190 180 ----**<<<-----XXXXXXX***<<---**<<<----XXXXXXXX**<<-160

SUBSTITUTE SHEET (RULE 26)





GMVFELANSIVLPFDCRDY	XXX <xxxxxx< th=""><th>640 650 SLFSAVKNFTEIASKFSERL</th><th>-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</th><th>690 700 </th><th>******</th><th>740 750 </th><th>XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</th></xxxxxx<>	640 650 SLFSAVKNFTEIASKFSERL	-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	690 700 	******	740 750 	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
LYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY	X-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	610 620 630 640 650 AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERL	XXXXX***X	660 670 680 690 700 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY	XXXXXXXXXXX	710 720 730 740 750 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA	XXXXXXX*****XXXXXXX
LYHSVYETY	XXX	61 AVVLRKYAL	-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	66 QDFDKSNP1	XX>>>** XX>>>**	71 AGESFPGIY	

22/48 FIGURE 15A

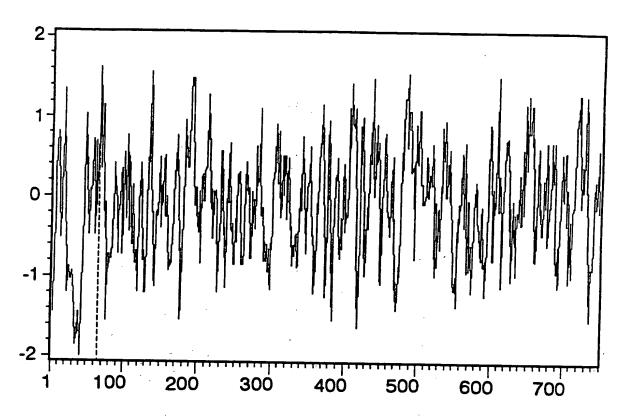


FIGURE 15B

Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

-> This is the value recommended by the authors The averaging group length is: 6 amino acids. The method used is that of Hopp and Woods.

The three highest points of hydrophilicity are:

Asp-Glu-Leu-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu Lys-Ser-Pro-Asp-Glu-Gly 68 137 487 to 132 482 From From From 1.62 1.57 1.55

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point: gave a proportion of 33% of incorrect predictions.

SUBSTITUTE SHEET (RULE 26)

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opt 321 311 266	321	A F	H. H.O	D & 0
init1 120 164 145	120	70 CCAGGTT ::::: CCAGGCT	30 CCAAGTAT :: :: CCCCACAT 1100	90 GGTGGCTC : :: SATGGAGA
initn 203 164 145	203	1070 TCACACC	1130 :GGTCTTCC/ :: :: :: GGACTACC/	1190 AAAATGGGTGG :::::::: AAAATGGATGG
FIGURE 16-1 c scores are: G.gallus mRNA for transferrin receptor Rat transferrin receptor mRNA, 3' end. Human transferrin receptor mRNA, complete cd	G.gallus mRNA for transferrin receptor identity in 717 nt overlap	1020 1030 1040 1050 1060 1070 TGTCCAGCGTGGAATATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA ::::::::::::::::::::::::::::::::	1080 1090 1100 1110 1120 1130 CCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGGGCTGTTGGTCTTCCAAGTAT :::::::::::::::::::::::::::::::::	1140 1150 1160 1170 1180 1190 TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAATGGGTGGCTC :::::::::::::::::::::::::::::
The best CHKTFER RATTRFR HUMTFRR	CHKTFER 51.9%	pmsgen CHKTFE	pmsgen CHKTFE	pmsgen CHKTFE

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1200 1210 1220 1230 1240 1250 AGCACCACCAGATAGCAGCTGGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG :: :: :: :: :: :: :: :: :: :: :: :: ::	70 1280 1290 1300 1310 CTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT :::::::::::::::::::::::::::::::	1320 1330 1340 1350 1360 1370 GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	1380 1390 1400 1410 1420 1430 CATTCTGGGAGGTCACCGGGACTCATGGGTGTTTTGGTGGTATTGACCCTCAGAGTGGAGC : :::::::::::::::::::::::::::::::::::
1240 AAAGTGCCCTAC. : :: CATTCCTGT	1300 ATGCACATCCA : : : : CTAGATGTGAA 0 1250	1360 GGAGCAGTGGA ::: ::: GGATTTGAAGA 0 1310	0 1420 TGGTGGTATTGA :::::::
AGGAAGTCTC:::	1290 AAAAGTCAAGATGCAC :: :: : : : : : : : : : : : : : : : :	1350 FACTCTCAGAG : :: :: : FGCTATCCAGG	1410 TTGGGTGTTTG:::::::::::::::::::::::::::
1220 GCAGCTGGAGAGG : :::::: GGTTGGAAAGG	1280 FTTCTACACAA : : : : GCCAGA-TA	1340 TGTGATAGGTAC : :::: CATCTTCGGTGC	0 1400 1 CACCGGACTCATGGGTG :: :::::::: CAGAGACTCCTGGGGC 40 1350
1200 1210 AGCACCACCAGATA(::::::: CACATGCTCTGA-A(12 ACTGGAAA : ::: : 3CAGGAGA	1320 1330 GACAAGAATTTACAA : :: :: :: CAGGAAGATTCTGAA 1270 1280	1390 TGGGAGGTCA : ::: :: TTGGAGCCCA
		1320 GACAA : : CAGGA 1270	1380 CATTC : TGTGA 1330
pmsgen CHKTFE	DIMSGEN CHKTFE (H) TEEHS ETUTITSBU	pmsgen CHKTFE	pmsgen CHKTFE
Si	ubstitute sheet (r	OLL 20)	

FIGURE 16-3

08/466381

	26/	48	. 60 \ 40
1450 1460 1470 1480 1490 TTCATGAAATTGTGAG——GAGCTTTGGAACACTGAAAAGGAAGGGTGGAG: ::::::::::::::::::::	1500 1510 1520 1530 1540 1550 pmsgen ACCTAGAACTTTTGTTTTGCAAGCTGGGATGCAGAACTTTTGGTTC :::::::::::::::::::::::::::::	1570 1580 1590 1600 1610 3CAGAGGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAA ::::::::::::::::::::::::::::	1630 1640 1650 1660 1670 TCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG : : : : : : : : : : : : : : : : : : :
1440 1450 AGCTGTTGTTCATGA :::::::::::::::::::::::::::::::::::	1500 ACCTAGAAGAAC ::::::: ACCGAGGCGAAG 1450	1560 TACTGAGTGGG :::::::: TACTGAATGGG	1620 TGC-TGACT :::: -GCTTGGAT
14 pmsgen AG : CHKTFE TG	pmsgen AC :: CHKTFE AC	pmsgen TA :: CHKTFE TA	pmsgen TC 8 CHKTFE -(
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SUBSTITUTE SHEET (RULE 26)

1730 FTTGAAGGC : :: :: FCAGAGAGC 1680	1790 SCATGCCC SGCCTGGA	
1720 SATGAAGGCT' : :: :: SCAGCAGTCT' 1670	1780 AGTTCAGTG	1720 1730
1690 1700 1710 1720 1730 ACAACCTAACAAAGGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC : : : : : : : : : : : : : : : : : : :	1770 CCTTCCCCAG	1720
1700 CAAAAGAGCTG : : : : : : : : TGAAGGGGGTG	1760 TAAAAAAAGT : : CAGACTGGGT	1710
1690 CACAACCTAAC : : : GGAGTATTAT	AAAGTTGGACTAAAA : : : : : : : : : : : : : : : : : :	1700
1680 1690 1700 1710 1720 1730 TACAGCTTGGTACAAACCAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTTGAAGGC :::::::::::::::::::::::::::::::::	pmsgen AAATCTCTTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC ::::::::::::::::::::::::::::::::::	0601
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1GURE 16-5

m	- 1	\CT
164	TGGCT : : : TAGAT	0 ATG ATGT?
164	1250 rgttggacc : : : gttggaata	1310 CTCT-ACCAA :: : ::: CTGTGAACAA
3' end.	AGCTGGAGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTT- :::::::::::::::::::::::::::::::::::	1280
cor mRNA,	1230 AGTCTCAAAG	1290 1290 AAGTCAAGAT : ::: :: SAATCAAAAT
ferrin receptor mRNA, 3' end 560 nt overlap	1220 TGGAGAGGAA CAAAAACATG	630 1280 CTACACAAAA ::: ACTTTCACAC
	1210 AGATAGCAGC AAAAGCTATT	620 1270 TACTGGAAACTTTT : :: :: TCATGTAAGCTGGA
RATTRER Rat trans 55.5% identity in	1210 pmsgen CCACCAGATAGCA RATTRF TGCAGAAAAGCTA	610 620 630 640 650 650 650 650 650 650 650 1260 1270 1280 1290 1300 1310 1316
		HEET (RULE 26)

FIGURE 16-6

	PCT/US93/10624
29/48	08/466381
GGGCCCTGGT-GTTGCGAAGTCCAGTG 830 840 GCTTTGGAACA-CTGAAAAAGGAA GTATTCTCAGATATGATTTCAAAAGAT 890 900	1520 1530 1540 GCAAGCTGGGATGCAGAATTTTGGTCTT :::::::::::::::::::::::::::::
TTTGO 0 GGA(CAA(880	15 GCA GCC 940

pmsgen ---AAGTGACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGGAGTGGAACCAGACAG RATTRF GAAAGAAACAAGAATACTTAACATCTTTGGCGTTATTAAAGGCTATGAGGAACCAGACCG pmsgen ATATGTCATTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAG RATTRF CTACATTGTAGTAGGAGCCCAGAGAGACGC pmsgen T-GGAGCAGCTGTTGTTCATGAAATTGTGA RATTRF TGGGAACAGGTCTT-CTGTTGAAACTTGCC GGGTGGAGACCTAGAAGAACAATTTTGTTT GGATTTAGACCCAGCAGGAGTATTATCTTT pmsgen RATTRF

SUBSTITUTE SHEET (RULE 26)

	- , -	
1600 GTGGCGTG : : GCTTTC 1020	1660 GATTGTAC : : TCTGCCAG 1080	1720
1590 CTTCAAGAGC : :: :: CATCTAAAG-	1650 TCTGAGAGTT : : :: CTTCAAGGTT 1070	1710
1580 1580 1000 1000 1580 1000 1010	0 1640 1650 1660 GAAGGAAACTA-CACTCTGAGAGTTGATTGTA ::::::::::::::::::::::::	1700
1550 1560 1570 1580 1590 1600 CTTGGTTCTACTGAGTGGCCAGAGGAATTCAAGACTCCTTCAAGAGCGTGGCGTG	163 ATA CGT 050	1690
1560 CTGAGTGGGC ::::::: CTGAGTGGCT 980	1620 ATGCTGACTCATCT ::::::::	ואאו
1550 18 CTTGGTTCTACT :::::::: GTTGGTCCGACTC	1610 pmsgen GCTTATATTAATG :::: ::::: RATTRF ACTTACATTAAT- 1030	1670
pmsgen RATTRF	pmsgen RATTRF	
SUBSTITUTE S	SHEET (RULE 26)	

pmsgen ACCGCTGATGTACAGCTTGGTACACAAACCAAAAGAGGCTGAAAAGC-CCTGATGAAG

ATACACTTATGGGGAAGATAATGCAGGA-1100 1120

RATTRF

	31	/48	
1730 1770 pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAAGTCCTTCCCAG ::::::::::::::::::::::::::::::::::	1190	AGTICAGIGGCAIGCCAGGAIAAGCAAATIGGGAICTGGAAATGATTIGGGTGTTTT	CATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC
1750 AGTTGGACTAAAAAAGTG : :::: :: :::: :	1180	GAAATGATTT	GAATCCCAGC 1240
1750 AGTTGGA : ::::	1170	ATTGGGATCTG	rgcatattcag 1230
1740 TCTTTAT-GAA :::::::	1160	GATAAGCAAI	CCCTTTTCT
1730 1740 TTGAAGGCAAATCTCTT' ::::::::::::::::::::::::::::::::	1150	GCATGCCCAG	ATGCTGCATI 1210
1730 GCTTTGAAGG ::::::	1140	AGTTCAGTG	RATTRF CCTTGGACAATGCTG
		pmsgen	
S	UBSTITUT	e sheet	RULE 28

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145	1230 1240 1250 1260 1270 pmsgen AGGAAGTCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC : : : : : : : : : : : : : : : : : : :	1280 1290 1300 1310 1320 1330 pmsgen AAAAAGTCAAGATGCACTC-CACTCT-ACCAATGAAGTGACAAGAATTTACAA : :::: ::::::::::::::::::::::::::::	1340 1350 1360 1370 1380 1390 pmsgen TGTGATACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGAGGTCA : :::::::::::::::::::::::::::::::::::	1400 1410 1420 1430 1440 1450 pmsgen CCGGGACTCATTGGTGGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATG ::::::::::::::::::::::::::::::::::::
145	1270 AACTTT : GGATGG 1190	1320 AAGTGACAAGAATTT :::::::: AAGAGATAAAAATTC 0	1380 13 TTATGTCATTCTGGGAGG ::::: : :::: TATGTTGTAGTTGGGGC	1440 AGCTGTTC ::::: AGCTCTCC
ල ග	rgga :::: rgta	13 3TGA : ::	13 3TCA :: 3TTG	AGCA ::
pleto	60 TTAC-7 ::: CTACA7	AAC ::8 TGAAAC	0 GATATC :::: ACTATC 1300	1430 1440 CCTCAGAGT-GGAGCAGCT : : : : : : : : : : : : : : : : : : :
COE	1260 GCTTT ::: ACTCT	TGCT	1370 ACAGA : ATCAC	1430 AGAG' : :
Human transferrin receptor mRNA, complete cd lentity in 464 nt overlap	50 1260 1 GGACCTGGCTTTAC-TGGAA : : : : : : : : : : : : : : : : : : :	1280 1290 1300 1310 pmsgen AAAAAGTCAAGGTGCACATC-CACTCT-ACCAATG- : :::: : :::: : :::::::::::::::::::::	1360 1370 AGTGGAACCAGACAG :::::::: FGTAGAACCAGATCA	0 GACCCTC : :: AAATC-C 1350
ptorap	1250 GTTGG2 TGGAAZ	1310 -CACTCT-ACCAATG :::::::::::::::::::::::::::::::::::	1360 GTGGA :: :: GTAGA	1420 ATTGACC : : GCAAAA1
rin recept nt overlap	ACAAT CTGAC 60	CACT	SAGCA SCTTT 80	0 TGGTGGTA1 :::::: TGGAGCTG0
rrin nt	1240 CCCTAC CCCTCT	1300 CATC-CA : : : AAGCTCA	1350 CAGAGGA(: ::: TAAAGGC	1410 GTTTGGT ::: CCCTGGA 1340
nnsfe 1 464	AAGTG ACTGT	TGCA::	TTCTC:	36GGC
n tra ty ir	1230 ICTCAA AGGAGA	1290 CAAGA : : AAGAA 1210	340 AGGTAC :: TGGAGT	00 rcarg :::: GCATG 1330
Human transfe identity in 464	13 AAGT	AAAAGT :::: SAAAGCZ	1340 GATAGG : :: CTTTGG	1400 GGGACTCATGGG : :: :::: GAGATGCATGGG
jq	n AGG R TAT	280 n AAA : : R AGA 1200	n TGT : R CAT 1260	n CCG : R GAG 1320
HUMTFRR 54.3%	sgen MTFR	1280 sgen A : MTFR A	sgen MTFR	sgen MTFR 13
3	md HU	md	nd HO	md

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FIGURE 16-1

pmsgen AAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAACAA :::::::::::::::::::::::::::::	pmsgen TTTTGTTTGCAAGCTGGGATGCAGAATTTGGTCTTCTTGGTTCTACTGAGTGGCAG ::::::::::::::::::::::::::::::::::	1570 1580 1590 1600 1610 1620 pmsgen A-GGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCT :::::::::::::::::::::::::::::::	1630 1640 1680 ATAGAAGGAAACTACACTCTGAGTTGATTTGTACACCGCTGATGTACA-GCTTGGT-AC : : : : : : : : : : : : : : : : : : :			
pmsgen AAAT::: HUMTFR AACT	1510 pmsgen TTTTG ::: HUMTFR TTATC	1570 pmsgen A-GG : :: HUMTFR AGGG	1630 pmsgen ATAG : HUMTFR GTTC			
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FIGURE 16-11

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35/48 **FIGURE 17A**



FIGURE 17B

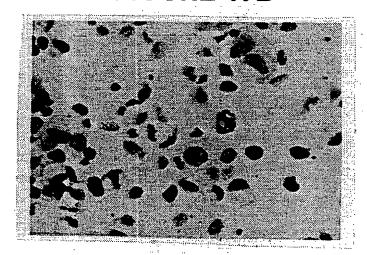
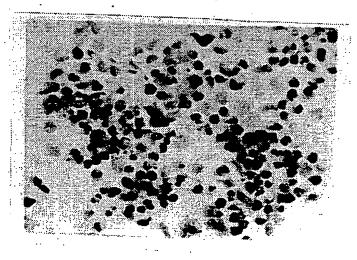


FIGURE 17C



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FIGURE 18

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FIGURE 19

1 2 3 4

200 kDa ---

100 kDa ---

69 kDa ----

— PSM

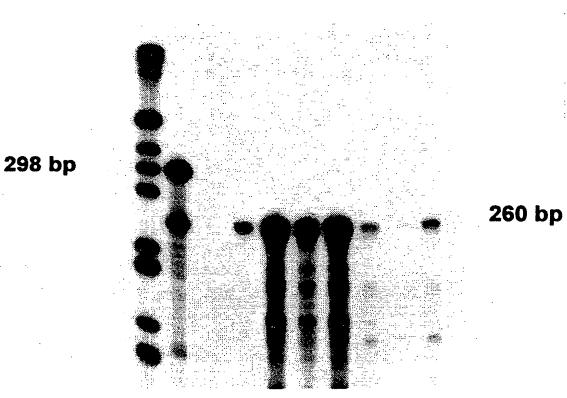
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FIGURE 20

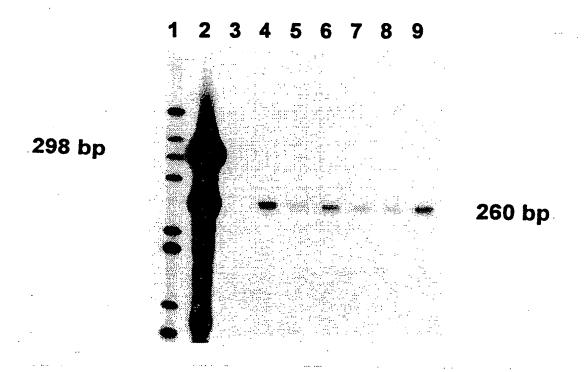
400

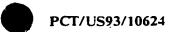
39/48 FIGURE 21

1 2 3 4 5 6 7 8 9 10



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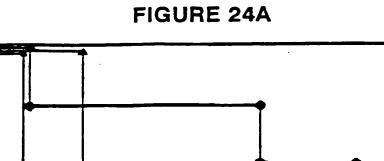
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CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED	
LNCap			++	ND	
HUMAN PROSTATE			++	ND	
A9 (FIBROSARCOMA)	NO	NO	-	-	
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT	
AT6.1 (RAT PROSTATE)	NO	YES		-	
AT6.1-11-c11	YES	NO	+	++	
AT6.1-11-c12	NO	YES	-	-	
R1564 (RAT MAMMARY)	NO	YES	-	-	
R1564-11-c14	YES	YES	-	+	
R1564-11-c15	YES	YES	_	REPEAT	
R1564-11-c16	YES	YES	_	ND	
R1564-11-c12	YES.	YES	ND	+	

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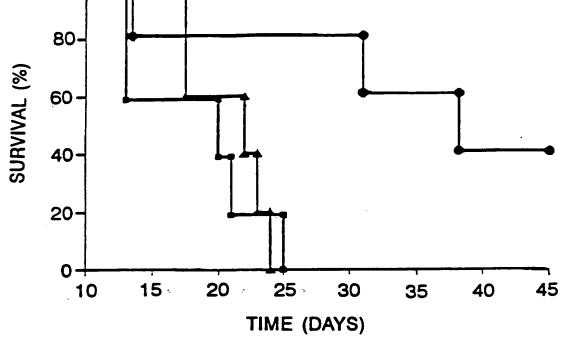
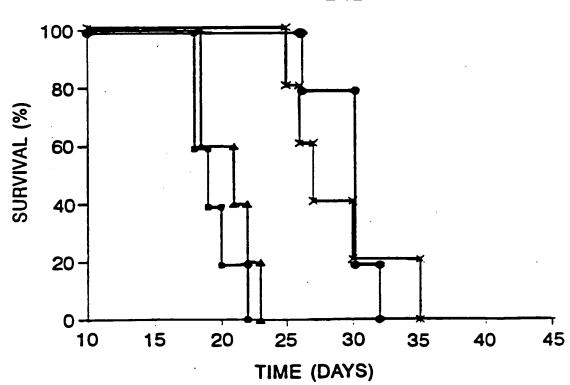


FIGURE 24B



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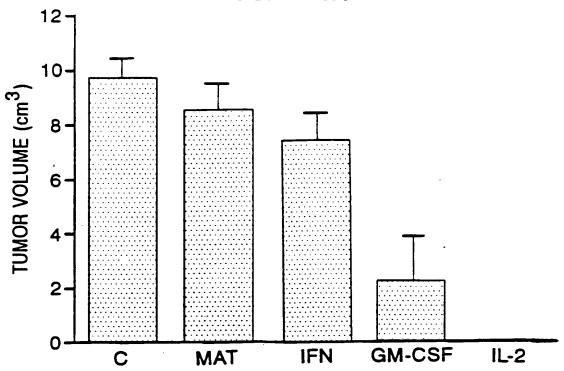
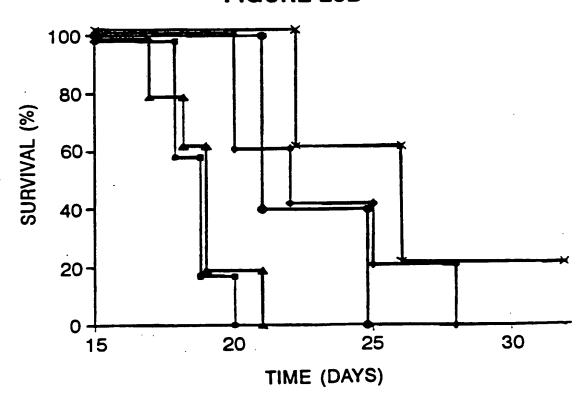
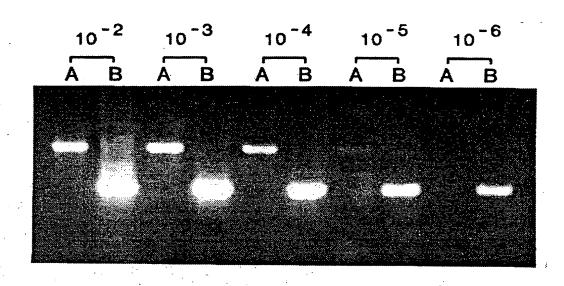


FIGURE 25B



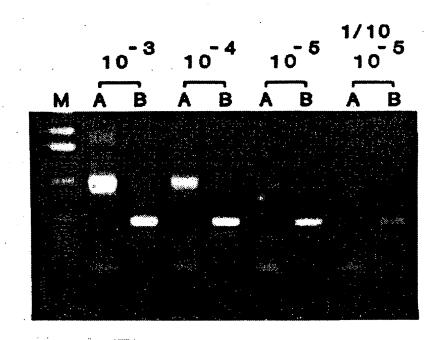
SUBSTITUTE SHEET (RULE 26)

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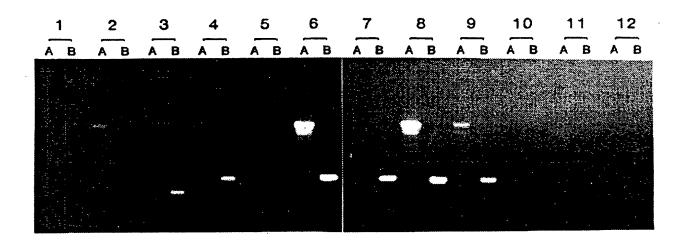


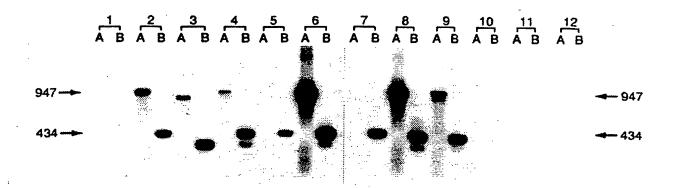
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FIGURE 30									
Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR			
1	T2NxMo	None	8.9	0.7	_	+			
2	T2NoMo	RRP 7/93	6.1	_	-	+			
3	T2CNoMo	PLND 5/93	4.5	0.1	_	+			
4	T2BNoMo	RRP 3/92	NMA	0.4	_	+			
5	T3NxMo	Proscar + Flutamide	51.3	1.0	_	+			
6	Recur T3	I-125 1986	54.7	1.4	-	+			
7	T3ANoMo	RRP 10/92	NMA	0.3	_	+			
8	T3NxMo	XRT 1987	7.5	0.1	- ·	- ·			
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-			
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	`+	+			
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+			
12	T2NoMo	RRP 8/91	NMA	0.5	_	+			
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-			
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	_			
15	D1	Proscar + Flutamide	20.8	0.5	_	-			
16	T2CNoMo	RRP 4/92 SUBSTITUTE SH	O.1 HEET (RULE	0.3 26)	-	-			